

Sequence error report

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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu May 03 16:48:36 EDT 2007

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Reviewer Comments:

<210> 4

<211> 6223

<212> DNA

<213> crt gene

<400> 4

The <213> response is invalid. Per 1.823 of Sequence Rules, the only valid <213> responses are: "Artificial Sequence," "Unknown," or the Genus/species. FYI: if this is an Artificial Sequence, then "crt gene" would be an insufficient explanation (please explain the source of the genetic material in the <223> response).

Same type of error in sequences 5-16

Application No: 10551508 Version No: 1.0

Input Set:

Output Set:

Started: 2007-05-03 16:08:57.906
Finished: 2007-05-03 16:08:58.290
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 384 ms
Total Warnings: 4
Total Errors: 0
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

ErrCode **Error Description**

W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)

SEQUENCE LISTING

<110> KIM, Young Tae
LEE, Jae Hyung

<120> Gene involved in the biosynthesis of carotenoid and marine
microorganism, paracoccus haeundaesis, producing the
carotenoid

<130> 428.1056

<140> 10551508

<141> 2007-05-03

<150> US 10/551,508

<151> 2005-09-29

<150> PCT/KR2004/000752

<151> 2003-03-31

<150> KR2003-20222

<151> 2003-03-31

<150> KR2003-20023

<151> 2003-03-31

<160> 18

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<213> Artificial Sequence

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<223> reverse primer for Paracoccus haeundaesis 16S rDNA

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<212> PRT
<213> crtW amino acid

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Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Phe Ile Ala
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His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Gly Asn
65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Thr Gly Thr
100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe

165

170

175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

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Thr Ala

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<211> 489

<212> DNA

<213> crtZ gene

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Gly Trp His Lys Ser His His Glu Glu His Asp His Ala Leu Glu Lys
 35 40 45

Asn Asp Leu Tyr Gly Leu Val Phe Ala Val Ile Ala Thr Val Leu Phe
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Thr Val Gly Trp Ile Trp Ala Pro Val Leu Trp Trp Ile Ala Leu Gly
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Met Thr Val Tyr Gly Leu Ile Tyr Phe Val Leu His Asp Gly Leu Val
 85 90 95

His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr Ala Arg
 100 105 110

Arg Leu Tyr Gln Ala His Arg Leu His His Ala Val Glu Gly Arg Asp
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His Cys Val Ser Phe Gly Phe Ile Tyr Ala Pro Pro Val Asp Lys Leu
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Arg Thr

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